MNSTPSKLLPIDKHSHLQLQPQSSSASIFNSPTKPLNFPRTNSKPSLDPNSSSDT
YTSEQDQEKGKEEKKDTAFQTSFDRNFDLDNSIDIQQTIQHQQQQPQQQQQLS
QTDNNLIDEFSFQTPMTSTLDLTKQNPTVDKVNENHAPTYINTSPNKSIMKKATPK
ASPKKVAFTVTNPEIHHYPDNRVEEEDQSQQKEDSVEPPLIQHQWKDPSQFNYS
DEDTNASVPPTPPLHTTKPTFAQLLNKNNEVNSEPEALTDMKLKRENFSNLSLDE
KVNLYLSPTNNNNSKNVSDMDSHLQNLQDASKNKTNENIHNLSFALKAPKNDIEN
PLNSLTNADISLRSSGSSQSSLQSLRNDNRVLESVPGSPKKVNPGLSLNDGIKGF
SDEVVESLLPRDLSRDKLETTKEHDAPEHNNENFIDAKSTNTNKGQLLVSSDDHL
DSFDRSYNHTEQSILNLLNSASQSQISLNALEKQRQTQEQEQTQAAEPEEETSFS
DNIKVKQEPKSNLEFVKVTIKKEPVSATEIKAPKREFSSRILRIKNEDEIAEPADIHP
KKENEANSHVEDTDALLKKALNDDEESDTTQNSTKMSIRFHIDSDWKLEDSNDG
DREDNDDISRFEKSDILNDVSQTSDIIGDKYGNSSSEITTKTLAPPRSDNNDKENS
KSLEDPANNESLQQQLEVPHTKEDDSILANSSNIAPPEELTLPVVEANDYSSFND
VTKTFDAYSSFEESLSREHETDSKPINFISIWHKQEKQKKHQIHKVPTKQIIASYQQ
YKNEQESRVTSDKVKIPNAIQFKKFKEVNVMSRRVVSPDMDDLNVSQFLPELSE
DSGFKDLNFANYSNNTNRPRSFTPLSTKNVLSNIDNDPNVVEPPEPKSYAEIRNA
RRLSANKAAPNQAPPLPPQRQPSSTRSNSNKRVSRFRVPTFEIRRTSSALAPCD
MYNDIFDDFGAGSKPTIKAEGMKTLPSMDKDDVKRILNAKKGVTQDEYINAKLVD
QKPKKNSIVTDPEDRYEELQQTASIHNATIDSSIYGRPDSISTDMLPYLSDELKKP
PTALLSADRLFMEQEVHPLRSNSVLVHPGAGAATNSSMLPEPDFELINSPARNVS
NNSDNVAISGNASTISFNQLDMNFDDQATIGQKIQEQPASKSANTVRGDDDGLA
SAPETPRTPTKKESISSKPAKLSSASPRKSPIKIGSPVRVIKKNGSIAGIEPIPKATH
KPKKSFQGNEISNHKVRDGGISPSSGSEHQQHNPSMVSVPSQYTDATSTVPDE
NKDVQHKPREKQKQKHHHRHHHHHHKQKTDIPGVVDDEIPDVGLQERGKLFFR
VLGIKNINLPDINTHKGRFTLTLDNGVHCVTTPEYNMDDHNVAIGKEFELTVADSL
EFILTLKASYEKPRGTLVEVTEKKVVKSRNRLSRLFGSKDIITTTKFVPTEVKDTWA
NKFAPDGSFARCYIDLQQFEDQITGKASQFDLNCFNEWETMSNGNQPMKRGKP
YKIAQLEVKMLYVPRSDPREILPTSIRSAYESINELNNEQNNYFEGYLHQEGGDC
PIFKKRFFKLMGTSLLAHSEISHKTRAKINLSKVVDLIYVDKENIDRSNHRNFSDVL
LLDHAFKIKFANGELIDFCAPNKHEMKIWIQNLQEIIYRNRFRRQPWVNLMLQQQ
QQQQQQQSSQQ

FIG. 1

APPROVED BY DRAFTSMAN | O.G. FIG. CLASS | SUBCLASS

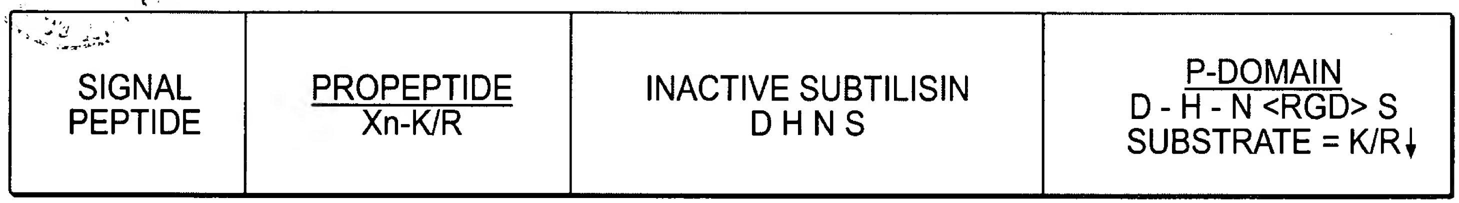
1 cccaaaaaag ataaaataaa aacaaaacaa aacaaaagta ctaacaaatt attgaaactt
61 ttaattttta ataaagaatc agtagatcta ttgttaaaag aaatgaactc aactccaagt
121 aaattattac cgatagataa acattctcat ttacaattac agcctcaatc gtcctcggca
181 tcaatattta attccccaac aaaaccattg aatttcccca gaacaaattc caagccgagt
241 ttagatccaa attcaagctc tgatacctac actagcgaac aagatcaaga gaaagggaaa
301 gaagagaaaa aggacacagc ctttcaaaca tcttttgata gaaattttga tcttgataat
361 tcaatcgata tacaacaaac aattcaacat cagcaacaac agccacaaca acaacaacaa
421 ctctcacaaa ccgacaataa tttaattgat gaatttttctt ttcaaacacc gatgacttcg
481 actttagacc taaccaagca aaatccaact gtggacaaag tgaatgaaaa tcatgcacca
541 acttatataa atacctcccc caacaaatca ataatgaaaa aggcaactcc taaagcgtca
601 cctaaaaaag ttgcatttac tgtaactaat cccgaaattc atcattatcc agataataga
661 gtcgaggaag aagatcaaag tcaacaaaaa gaagattcag ttgagccacc cttaatacaa
721 catcaatgga aagatccttc tcaattcaat tattctgatg aagatacaaa tgcttcagtt
781 ccaccaacac caccacttca tacgacgaaa cctacttttg cgcaattatt gaacaaaaac
841 aacgaagtca atctggaacc agaggcattg acagatatga aattaaagcg cgaaaatttc
901 agcaatttat cattagatga aaaagtcaat ttatatctta gtcccactaa taataacaat
961 agtaagaatg tgtcagatat ggatctgcat ttacaaaact tgcaagacgc ttcgaaaaac
1021 aaaactaatg aaaatattca caatttgtca tttgctttaa aagcaccaaa gaatgatatt
1081 gaaaacccat taaactcatt gactaacgca gatattctgt taagatcatc tggatcatca
1141 caatcgtcat tacaatcttt gaggaatgac aatcgtgtct tggaatcagt gcctgggtca
1201 cctaagaagg ttaatcctgg attgtctttg aatgacggca taaaggggtt ctctgatgag
1261 gttgttgaat cattacttcc tcgtgactta tctcgagaca aattagagac tacaaaagaa
1321 catgatgcac cagaacacaa caatgagaat tttattgatg ctaaatcgac taataccaat
1381 aagggacaac tcttagtatc atctgatgat catttggact cttttgatag atcctataac
1441 cacactgaac aatcaatttt gaatcttttg aatagtgcat cacaatctca aatttcgtta
1501 aatgcattgg aaaaacaaag gcaaacacag gaacaagaac aaacacaagc ggcagagcct
1561 gaagaagaaa cttcgtttag tgataatatc aaagttaaac aagagccaaa gagcaatttg
1621 gagtttgtca aggttaccat caagaaagaa ccagttctgg ccacggaaat aaaagctcca
1681 aaaagagaat tttcaagtcg aatattaaga ataaaaaatg aagatgaaat tgccgaacca
1741 gctgatattc atcctaaaaa agaaaatgaa gcaaacagtc atgtcgaaga tactgatgca
1801 ttgttgaaga aagcacttaa tgatgatgag gaatctgaca cgacccaaaa ctcaacgaaa
1861 atgtcaattc gttttcatat tgatagtgat tggaaattgg aagacagtaa tgatggcgat
1921 agagaagata atgatgatat ttctcgtttt gagaaatcag atattttgaa cgacgtatca
1981 cagacttctg atattattgg tgacaaatat ggaaactcat caagtgaaat aaccaccaaa
2041 acattagcac ccccaagatc ggacaacaat gacaaggaga attctaaatc tttggaagat
2101 ccagctaata atgaatcatt gcaacaacaa ttggaggtac cgcatacaaa agaagatgat
2161 agcattttag ccaactcgtc caatattgct ccacctgaag aattgacttt gcccgtagtg
2221 gaagcaaatg attattcatc ttttaatgac gtgaccaaaa cttttgatgc atactcaagc
2281 tttgaagagt cattatctag agagcacgaa actgattcaa aaccaattaa tttcatatca
2341 atttggcata aacaagaaaa gcagaagaaa catcaaattc ataaagttcc aactaaacag
2401 atcattgcta gttatcaaca atacaaaaac gaacaagaat ctcgtgttac tagtgataaa
2461 gtgaaaatcc caaatgccat acaattcaag aaattcaaag aggtaaatgt catgtcaaga
2521 agagttgtta gtccagacat ggatgatttg aatgtatctc aatttttacc agaattatct
2581 gaagactctg gatttaaaga tttgaatttt gccaactact ccaataacac caacagacca
2641 agaagtttta ctccattgag cactaaaaat gtcttgtcga atattgataa cgatcctaat

FIG. 2A

2701 gttgttgaac ctcctgaacc gaaatcatat gctgaaatta gaaatgctag acggttatca
2761 gctaataagg cagcgccaaa tcaggcacca ccattgccac cacaacgaca accatcttca
2821 actcgttcca attcaaataa acgagtgtcc agatttagag tgcccacatt tgaaattaga
2881 agaacttctt cagcattagc accttgtgac atgtataatg atatttttga tgatttcggt
2941 gcgggttcta aaccaactat aaaggcagaa ggaatgaaaa cattgccaag tatggataaa
3001 gatgatgtca agaggatttt gaatgcaaag aaaggtgtga ctcaagatga atatataaat
3061 gccaaacttg ttgatcaaaa acctaaaaag aattcaattg tcaccgatcc cgaagaccga
3121 tatgaagaat tacaacaaac tgcctctata cacaatgcca ccattgattc aagtatttat
3181 ggccgaccag actccatttc taccgacatg ttgccttatc ttagtgatga attgaaaaaa
3241 ccacctacgg ctttattatc tgctgatcgt ttgtttatgg aacaagaagt acatccgtta
3301 agatcaaact ctgttttggt tcacccaggg gcaggagcag caactaattc ttcaatgtta
3361 ccagagccag attttgaatt aatcaattca cctgctagaa atgtgctgaa caacagtgat
3421 aatgtcgcca tcagtggtaa tgctagtact attagtttta accaattgga tatgaatttt
3481 gatgaccaag ctacaattgg tcaaaaaatc caagagcaac ctgcttcaaa atccgccaat
3541 actgttcgtg gtgatgatga tggattggcc agtgcacctg aaacaccaag aactcctacc
3601 aaaaaggagt ccatatcaag caagcctgcc aagctttctt ctgcctcccc tagaaaatca
3661 ccaattaaga ttggttcacc agttcgagtt attaagaaaa atggatcaat tgctggcatt
3721 gaaccaatcc caaaagccac tcacaaaccg aagaaatcat tccaaggaaa cgagatttca
3781 aaccataaag tacgagatgg tggaatttca ccaagctccg gatcagagca tcaacagcat
3841 aatcctagta tggtttctgt tccttcacag tatactgatg ctacttcaac ggttccagat
3901 gaaaacaaag atgttcaaca caagcctcgt gaaaagcaaa agcaaaagca tcaccatcgc
3961 catcatcatc atcatcataa acaaaaaact gatattccgg gtgttgttga tgatgaaatt
4021 cctgatgtag gattacaaga acgaggcaaa ttattcttta gagttttagg aattaagaat
4081 atcaatttac ccgatattaa tactcacaaa ggaagattca ctttaacgtt ggataatgga
4141 gtgcattgtg ttactacacc agaatacaac atggacgacc ataatgttgc cataggtaaa
4201 gaatttgagt tgacagttgc tgattcatta gagtttattt taactttgaa ggcatcatat
4261 gaaaaacctc gtggtacatt agtagaagtg actgaaaaga aagttgtcaa atcaagaaat
4321 agattgagtc gattatttgg atcgaaagat attatcacca cgacaaagtt tgtgcccact
4381 gaagtcaaag atacctgggc taataagttt gctcctgatg gttcatttgc tagatgttac
4441 attgatttac aacaatttga agaccaaatc accggtaaag catcacagtt tgatctcaat
4501 tgttttaatg aatgggaaac tatgagtaat ggcaatcaac caatgaaaac aggcaaacct
4561 tataagattg ctcaattgga agttaaaatg ttgtatgttc cacgatcaga tccaagagaa
4621 atattaccaa ccagcattag atccgcatat gaaagcatca atgaattaaa caatgaacag
4681 aataattact ttgaaggtta tttacatcaa gaaggaggtg attgtccaat ttttaagaaa
4741 cgtttttca aattaatggg cacttcttta ttggctcata gtgaaatatc tcataaaact
4801 agagccaaaa ttaatttatc aaaagttgtt gatttgattt atgttgataa agaaaacatt
4861 gatcgttcca atcatcgaaa tttcagtgat gtgttattgt tggatcatgc attcaaaatc
4921 aaatttgcta atggtgagtt gattgatttt tgtgctccta ataaacatga aatgaaaata
4981 tggattcaaa atttacaaga aattatctat agaaatcggt tcagacgtca accatgggta
5041 aatttgatgc ttcaacaaca acaacaacaa caacaacaac aaagctccca acagtaattg
5101 aaaggtctac ttttgatttt tttaatttta attggcaaat atatgcccat tttgtattat
5161 cttttagtct aatagcgttt tcttttttc cagt

FIG. 2B

ACTIVATION OF "SUBTILISIN-LIKE" PROPROTEIN CONVERTASES



THE PROCESSING OR "P-DOMAIN" CLIPS THE PROPEPTIDE AT THE CARBOXY TERMINAL SIDE OF DIBASIC RESIDUES, THEREBY RELEASING THE PROPEPTIDE. EXPOSED D -H -N -S ACTIVE SITE RESIDUES ASSUME THE SUBTILISIN SERINE PROTEASE CONFORMATION.

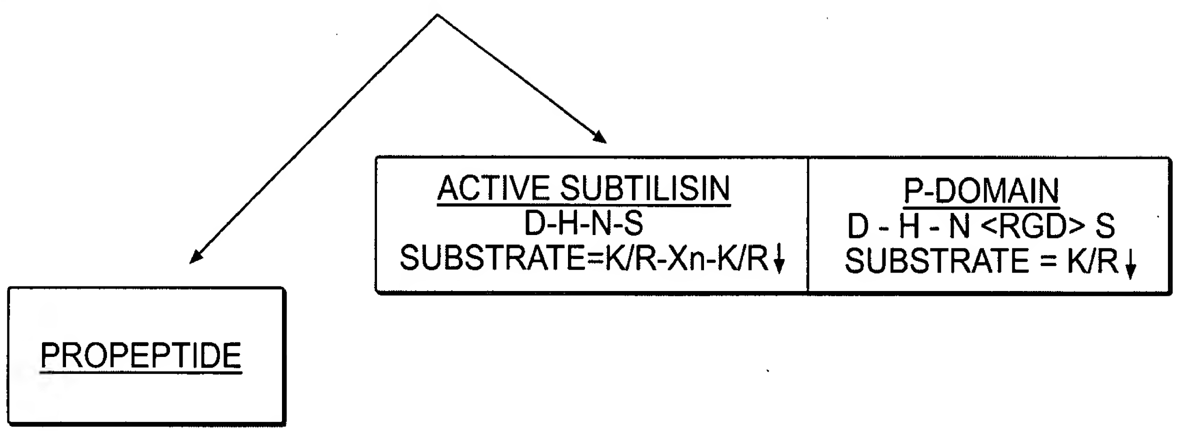


FIG. 3

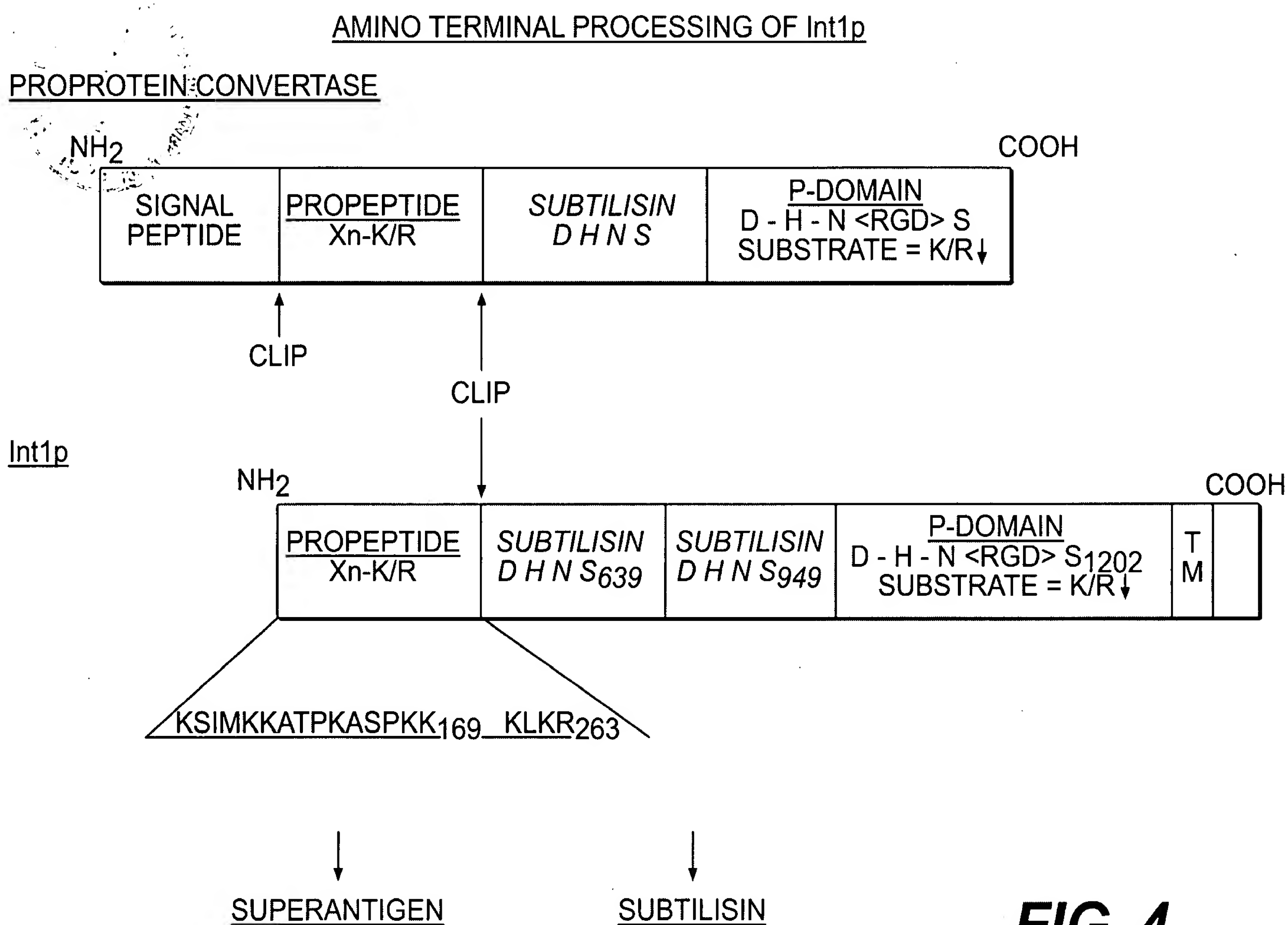

AMINO TERMINAL PROCESSING OF Int1p
PROPROTEIN CONVERTASE
NH2
COOH
SIGNAL PEPTIDE
PROPEPTIDE
Xn-K/R
SUBTILISIN
D H N S
P-DOMAIN
D - H - N <RGD> S
SUBSTRATE = K/R
CLIP
CLIP
Int1p
NH2
COOH
PROPEPTIDE
Xn-K/R
SUBTILISIN
D H N S639
SUBTILISIN
D H N S949
P-DOMAIN
D - H - N <RGD> S1202
SUBSTRATE = K/R
T
M
KSIMKKATPKASPKK169 KLKR263
SUPERANTIGEN
SUBTILISIN

FIG. 4

P DOMAIN SUBTILISIN MOTIFS

Kex2	D179	H213	N314	< R318GD >	S378 =	199aa
Furin	D355	H395	N479	< R498GD >	S555 =	200aa
Int1p	D1022	H1064	N1146	< R1149GD >	S1236 =	215aa
CD18	D290	H309	N351	< R397GD >	S490 =	200aa
C3	D1245	H1289	N1327	< R1393GD >	S1430 =	185aa
SpeB	D135	H159	N295	< R307GD >	S324 =	189aa
Fibrillin	D930	H971	N1052	< R1053GD >	S1129 =	199aa
EGF	D219	H286	N312	< R363GD >	S403 =	184aa
Fibronectin	D1365	H1396	N1488	< R1565GD >	S1565 =	200aa

FIG. 5

COMPARISON OF THE HIGH AFFINITY HEPARIN-BINDING SITE OF *MYCOBACTERIUM TUBERCULOSIS* HEPARIN-BINDING HEMAGGLUTININ ADHESIN (HBHA) WITH THE PROPOSED HEPARIN-BINDING SITE OF *CANDIDA ALBICANS* Int1p

HBHA	$\underline{K}_{180}$ AAA $\underline{KK}$ APA $\underline{KK}$ AAA $\underline{KK}_{195}$
Int1p	$\underline{K}_{155}$ SIM $\underline{KK}$ ATP $\underline{K}$ ASP $\underline{KK}_{169}$

FIG. 6

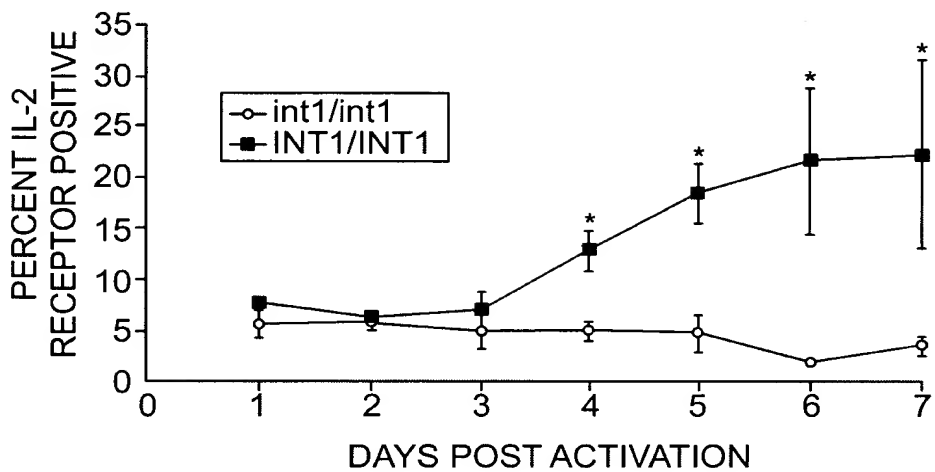

PERCENT IL-2
RECEPTOR POSITIVE
35
30
25
20
15
10
5
0
0
1
2
3
4
5
6
7
DAYS POST ACTIVATION
int1/int1
INT1/INT1
*

FIG. 7

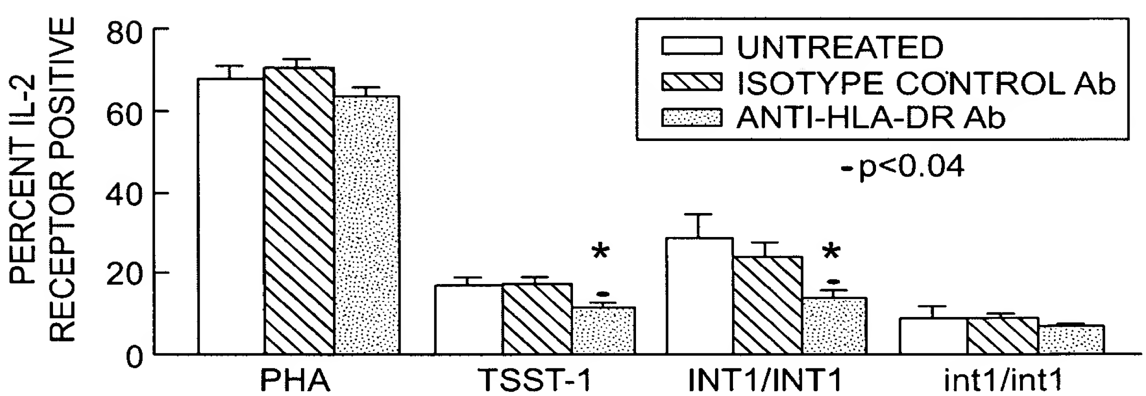

PERCENT IL-2
RECEPTOR POSITIVE
80
60
40
20
0
UNTREATED
ISOTYPE CONTROL Ab
ANTI-HLA-DR Ab
- p<0.04
*
PHA
TSST-1
INT1/INT1
int1/int1

FIG. 8

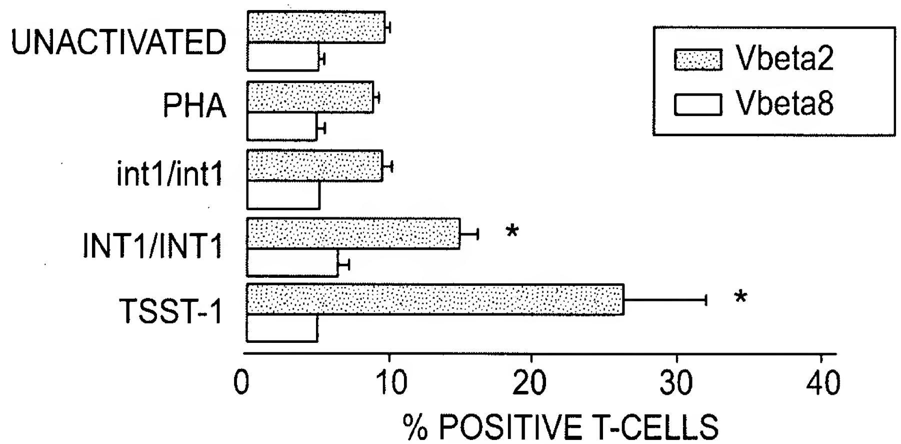


FIG. 9

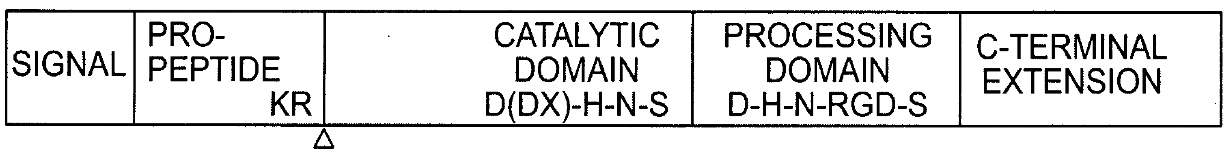


FIG. 10

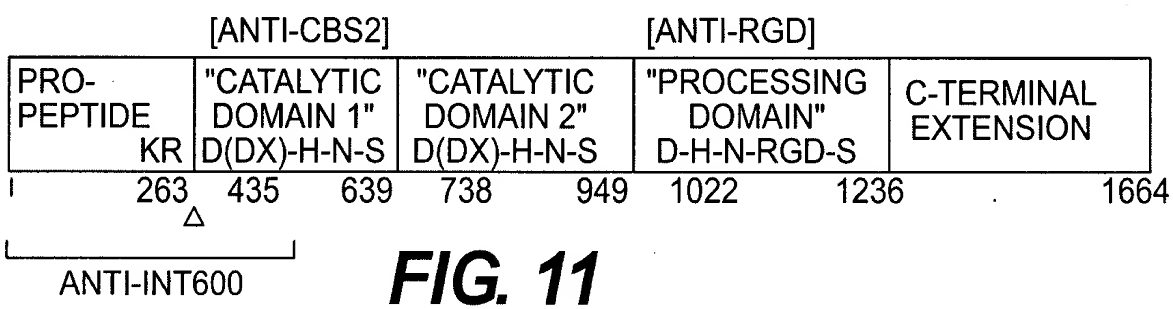


FIG. 11

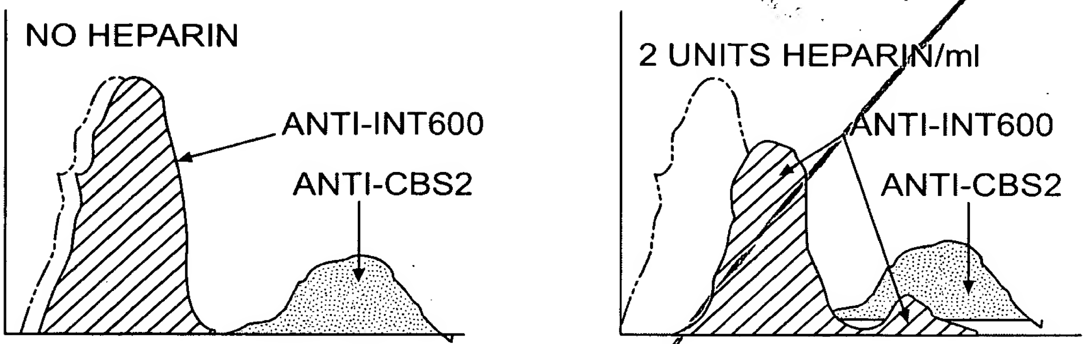

NO HEPARIN
ANTI-INT600
ANTI-CBS2
2 UNITS HEPARIN/ml
ANTI-INT600
ANTI-CBS2

FIG. 12

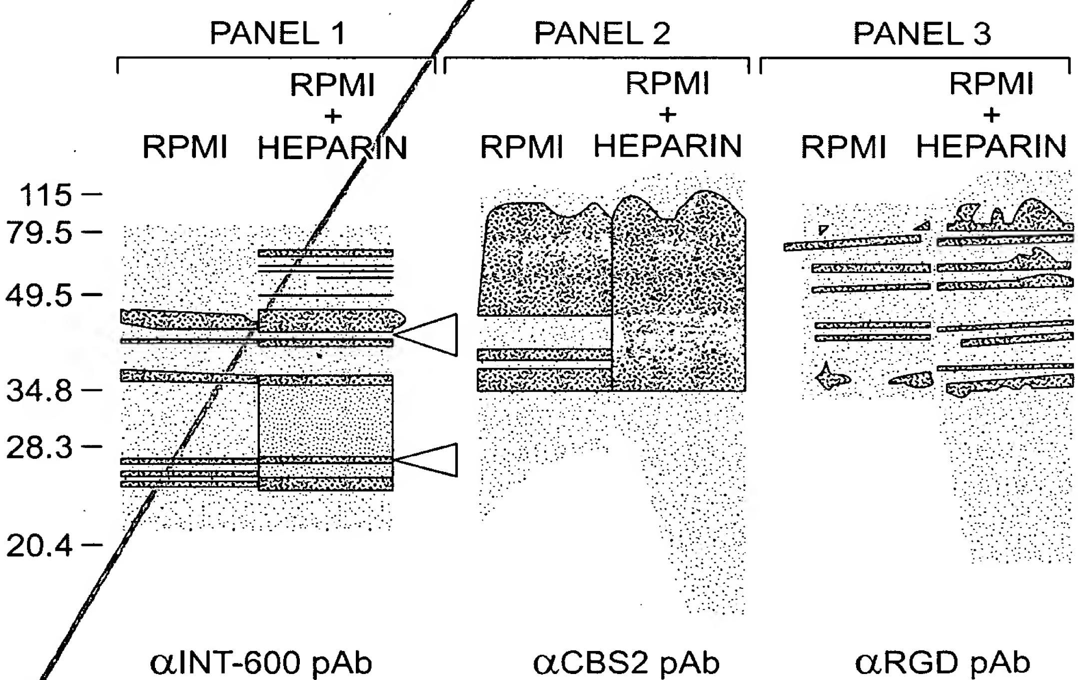

PANEL 1
PANEL 2
PANEL 3
RPMI
RPMI + HEPARIN
RPMI
RPMI + HEPARIN
RPMI
RPMI + HEPARIN
115
79.5
49.5
34.8
28.3
20.4
αINT-600 pAb
αCBS2 pAb
αRGD pAb

FIG. 13

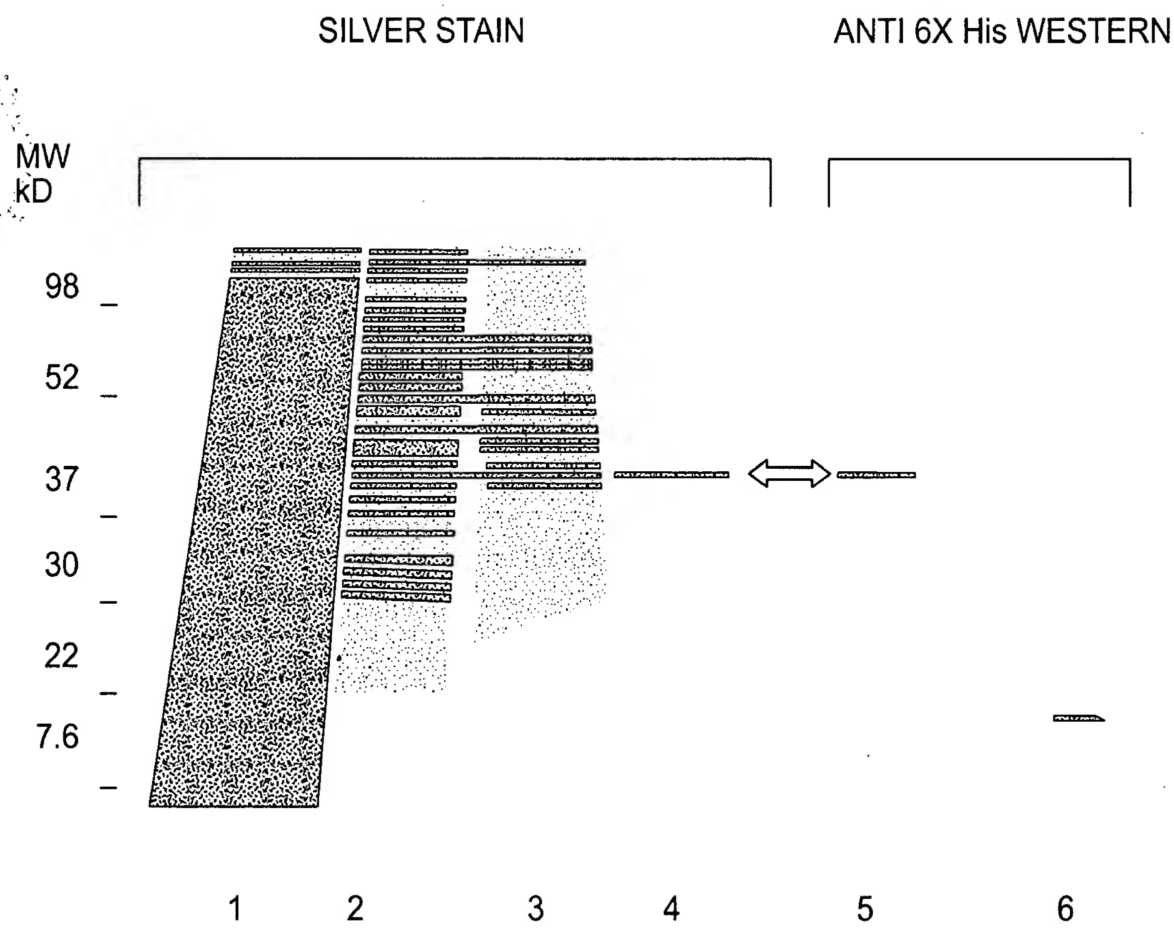


FIG. 14

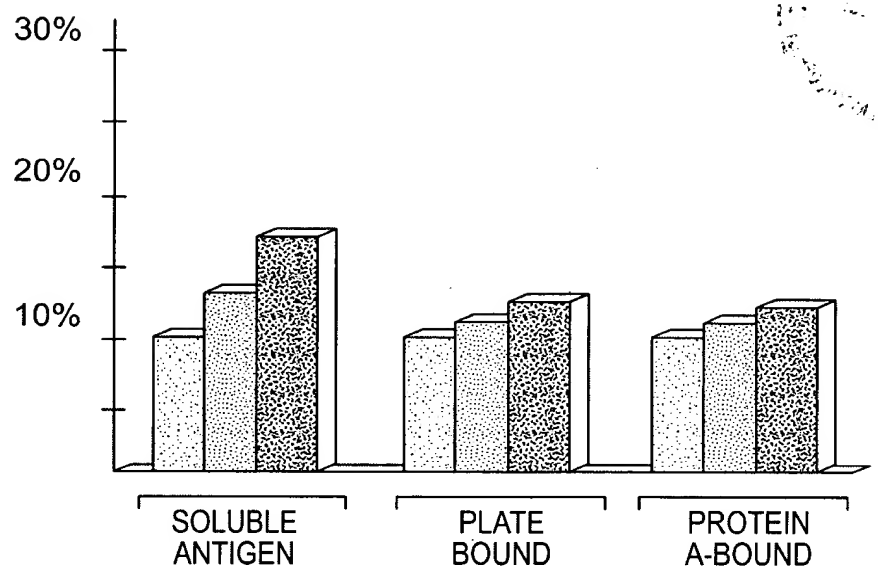

30%
20%
10%
SOLUBLE ANTIGEN
PLATE BOUND
PROTEIN A-BOUND

FIG. 15

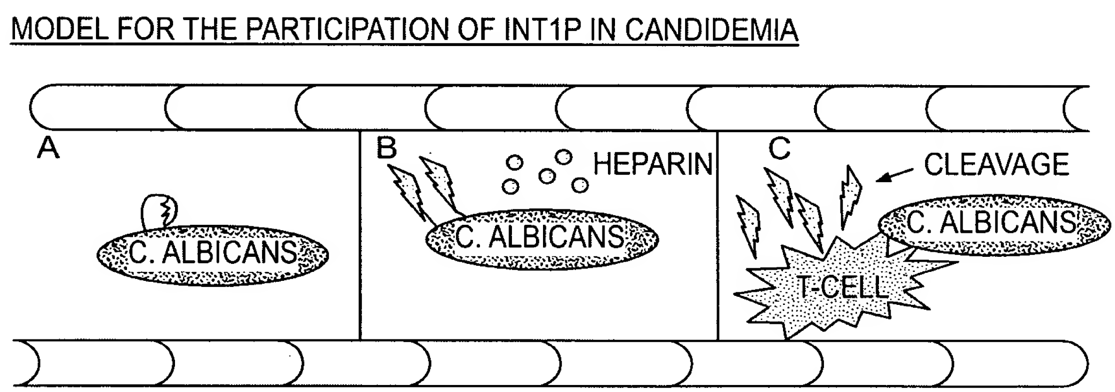

MODEL FOR THE PARTICIPATION OF INT1P IN CANDIDEMIA
A
C. ALBICANS
B
HEPARIN
C. ALBICANS
C
CLEAVAGE
C. ALBICANS
T-CELL

FIG. 16

MHC CLASS II-BINDING PEPTIDES

MAM $_{15}$F V Q N L - - N N V V F T N K E L E$_{31}$

Int1p $_{239}$F A Q L L N K N N E V - - N S E P E$_{254}$

FIG. 17

LINKAGE OF T LYMPHOCYTE TO ANTIGEN-PRESENTING CELL

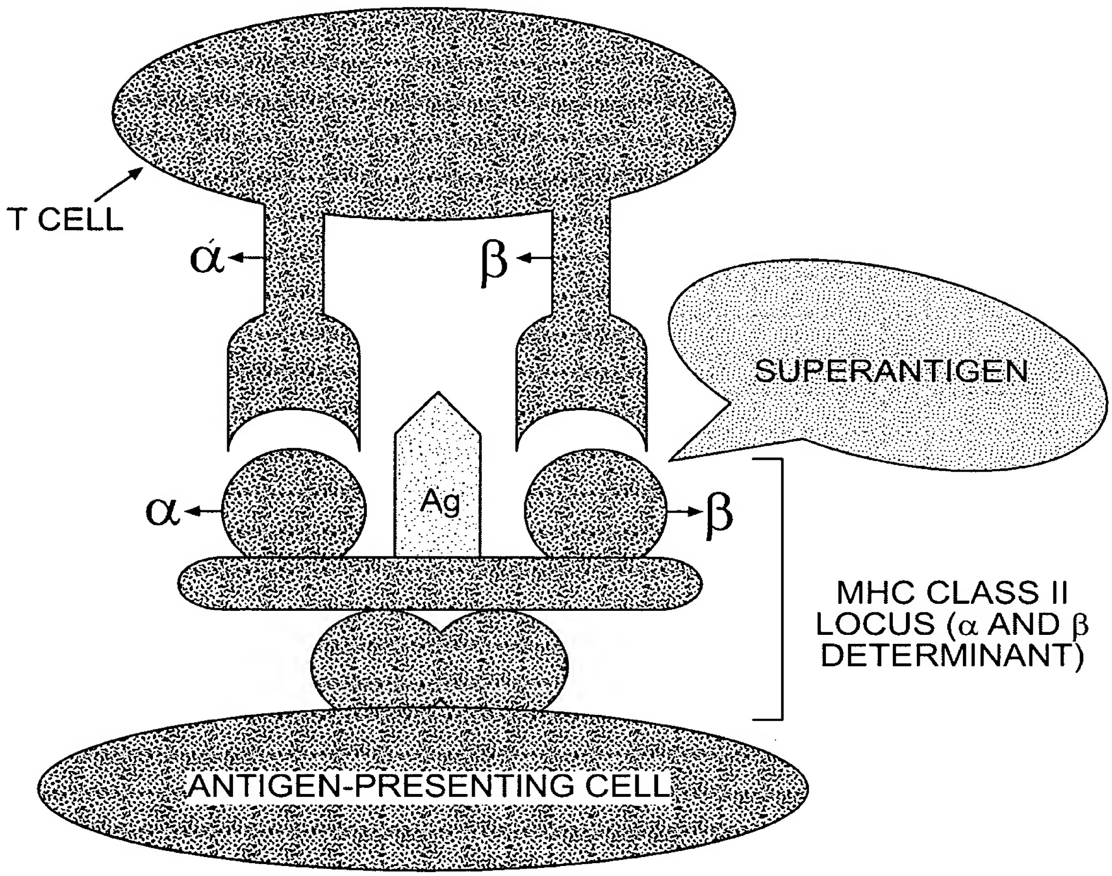


FIG. 18